

Abstract 7:

The fate of duplicated genes in the Interferon stimulated pathways in the tetraploid Common Carp

Annemiek Blasweiler^{1*}, Hendrik-Jan Megens^{1,2}, Geert Wiegertjes¹

¹ Aquaculture & Fisheries Group, Wageningen University & Research, The Netherlands

² Animal Breeding and Genetics Group, Wageningen University & Research, The Netherlands

* Corresponding author. E-mail: annemiek.blasweiler@wur.nl

After the event of a whole genome duplication, duplicated genes are often lost over time. In the common carp (*Cyprinus carpio*) the duplication event is so recent that most of the genome is still in duplicated state. Following interbreeding of two diploid species, the common carp contains two subgenomes from different ancestral origin and can be called an allotetraploid (n=50). Progressively, advances in next generation sequencing technology are providing methods to reliably characterize recently duplicated genomes. Here, we present a new carp genome assembly, combining Illumina short read sequencing, Nanopore long read sequencing and HiC, a proximity ligation method that captures the three-dimensional organizational structure of chromatin. This combination of methods allows the disentanglement of the two subgenomes to reflect the two ancestral, interbreeding species. Correct interpretation of ploidy effects on immune responses requires detailed knowledge of the degree of functional divergence between duplicated genes, and their role in molecular pathways. We zoomed in on interferon-stimulated genes (ISGs) commonly expressed in response to viral infection. Binding of interferon (IFN) to cell surface receptors initiates protein signalling pathways within the cell and leads to the expression of a subset of ISG genes involved in responses of the innate immune system. We show that the carp has an ancestral set of ISGs active on both sub genomes, suggesting a complex organization of immune responses not easily explained by single subgenome dominance.